

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03:  
1: uniprot\_sprot;\*  
2: uniprot\_trembl;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARES

| Result No. | Query      | Match length | DB ID        | Description                      |
|------------|------------|--------------|--------------|----------------------------------|
| 1          | 37556 99.9 | 731          | 1 KU86_HUMAN | P13010 h atp-depen               |
| 2          | 2971 79.0  | 732          | 2 Q60449     | Q60449 cricetulus                |
| 3          | 2971 79.0  | 732          | 2 060530     | 060530 mesocricetus              |
| 4          | 2939 78.1  | 732          | 2 080071     | Q80071 mus musculus              |
| 5          | 2937 78.1  | 731          | 2 Q8K1K7     | Q8K1K7 mus musculus              |
| 6          | 2932 78.0  | 732          | 2 Q9R169     | Q9R169 mus musculus              |
| 7          | 2922 77.7  | 732          | 2 Q6P7P8     | Q6P7P8 rattus norvegicus         |
| 8          | 2885 76.9  | 732          | 1 KU86_MOUSE | P27411 mus musculus              |
| 9          | 2865 76.2  | 708          | 2 Q8C4N6     | Q8C4N6 mus musculus              |
| 10         | 2748 73.1  | 683          | 2 Q8VIB0     | Q8VIB0 rattus norvegicus         |
| 11         | 2339 62.2  | 726          | 2 Q6DD59     | Q6DB89 xenopus laevis            |
| 12         | 2327 61.9  | 726          | 2 Q9W627     | Q9W627 xenopus laevis            |
| 13         | 1065 28.3  | 283          | 2 Q9CR15     | Q9CR15 mus musculus              |
| 14         | 698 18.3   | 138          | 2 Q6U1L6     | Q6U1L6 pan troglodytes           |
| 15         | 698 18.3   | 138          | 2 Q6U1L6     | Q6U1L6 macaca mulatta            |
| 16         | 595 15.6   | 683          | 2 Q8S563     | Q8S563 medicago truncatula       |
| 17         | 569 15.1   | 686          | 2 Q8S562     | Q8S562 phaseolus vulgaris        |
| 18         | 540.5 14.4 | 593          | 2 Q7Q190     | Q7Q190 anopheles gambiae         |
| 19         | 525 14.0   | 680          | 2 Q9FQ09     | Q9FQ09 arabidopsis thaliana      |
| 20         | 525 14.0   | 688          | 2 Q75IP6     | Q75IP6 oryza sativa              |
| 21         | 496 13.2   | 663          | 2 Q9C723     | Q9C723 arabidopsis thaliana      |
| 22         | 459 12.2   | 707          | 2 Q9LNP5     | Q9LNP5 arabidopsis thaliana      |
| 23         | 418 11.1   | 661          | 2 Q7RK73     | Q7RK73 neurospora crassa         |
| 24         | 402.5 10.7 | 145          | 2 Q9OZQ9     | Q9OZQ9 oryza sativa              |
| 25         | 344 9.1    | 726          | 2 Q6C7B9     | Q6C7B9 yarrowia lipolytica       |
| 26         | 342 9.1    | 695          | 2 Q9HGM8     | Q9HGM8 schizosaccharomyces pombe |
| 27         | 318.5 8.5  | 699          | 2 Q8MSM8     | Q8MSM8 drosophila melanogaster   |
| 28         | 318.5 8.5  | 699          | 2 Q9NGK6     | Q9NGK6 drosophila melanogaster   |
| 29         | 316.5 8.4  | 699          | 2 Q917M8     | Q917M8 drosophila melanogaster   |
| 30         | 309.5 8.2  | 904          | 2 Q9NK79     | Q9NK79 drosophila melanogaster   |
| 31         | 294.5 7.8  | 728          | 2 Q21829     | Q21829 caenorhabditis elegans    |

## ALIGNMENTS

| RESULT 1<br>KU86_HUMAN   | STANDARD: | PRT: | 731 AA. |
|--|-----------|------|---------|
| ID KU86_HUMAN  |           |      |         |
| AC P13010;   |           |      |         |
| DT 01-JAN-1990 (Rel. 13, Created)  |           |      |         |
| DT 01-FEB-1995 (Rel. 31, Last sequence update)   |           |      |         |
| DT 25-OCT-2004 (Rel. 45, Last annotation update)   |           |      |         |
| DB ATP-dependent DNA helicase II, 80 kDa subunit (Lupus Ku autoantigen protein p86) (Ku86) (86 kDa subunit of Ku antigen) (Thyroid-lupus autoantigen) (TLAA) (CTC box binding factor 85 kDa subunit)   |           |      |         |
| DB (CTCBP) (CTC85) (Nuclear factor IV) (DNA-repair protein xRCC5). Name=xRCC5; Synonyms=G22P2;   |           |      |         |
| GN Homo sapiens (Human); Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1]   |           |      |         |
| OC Sequence from N.A., and sequence of 3-21. [1]   |           |      |         |
| OX MEDLINE:89340410; PubMed:2160028;   |           |      |         |
| RN Yaneva M., Wen J., Ayala A., Cook R.; Sequence from N.A., and sequence of 3-21. [1]   |           |      |         |
| RP MEDLINE:89340410; PubMed:2160028;   |           |      |         |
| RX NCBITaxonID=9606;   |           |      |         |
| RA "cDNA-derived amino acid sequence of the 86-kDa subunit of the Ku antigen." [2]   |           |      |         |
| RT J. Biol. Chem. 264:13407-13411(1998).   |           |      |         |
| RL RN Sequence from N.A. [2]   |           |      |         |
| RX MEDLINE:90175380; PubMed:2308937;   |           |      |         |
| RA Mimori T., Ohosome Y., Hama N., Suwa A., Akizuki M., Homma M., Griffith A.J., Hardin J.A.; Isolation and characterization of cDNA encoding the 80-kDa subunit protein of the human autoantigen Ku (p70/p80) recognized by antibodies from patients with scleroderma-polymyositis overlap syndrome." [3]   |           |      |         |
| RT Casavant T.J., Scheetz T.E., Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C., Proc. Natl. Acad. Sci. U.S.A. 87:1777-1781(1990).   |           |      |         |
| RL RN Sequence from N.A. [3]   |           |      |         |
| RC Tissue:Uterus; MEDLINE:22388257; PubMed:12477932; DOI=10.1073/pnas.242603899;   |           |      |         |
| RX STRAUSBERG R.L., Feinold B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shemesh C.M., Schulz G.D., Altshul S.F., Zeeberg B., Buetow K.C., Schaeffer C.B., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin M.F., Casavant T.J., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.E., Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C., Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J., Bosak S.A., McElwan P.J., McKernan K.J., Malek J.A., Guanartane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton B., Ketten M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalak U., Smailus D.E., Schein J.B., Schein J.R., Jones S.J.M., Marra M.A.; [4] |           |      |         |

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OM protein - protein search, using sw model

Run on: August 17, 2005, 20:12:52 ; Search time 44 Seconds  
 1600.697 Million cell updates/sec

Title: US-10-768-030-1

Perfect score: 3761

Sequence: 1 MVRSGRKAAVYLCDMVGFTM.....GDATAAVFEERGGDVDLDLDMI 732

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\*

Maximum Match 100\*

Listing first 45 summaries

Database : PIR 79;\*

1: PIR2;\*

2: PIR2;\*

3: PIR3;\*

4: PIR3;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Match Length DB ID Description

| Result No. | Score | Query | Match | Length | DB     | ID | Description          |
|------------|-------|-------|-------|--------|--------|----|----------------------|
| 1          | 3761  | 100.0 | 732   | 2      | A32626 |    | Ku antigen 80K chain |
| 2          | 2971  | 79.0  | 732   | 2      | JC6099 |    | Ku autoantigen 86K   |
| 3          | 2893  | 76.9  | 732   | 2      | S26303 |    | Ku autoantigen 80K   |
| 4          | 459   | 12.9  | 707   | 2      | G96520 |    | protein F21D18.26    |
| 5          | 294.5 | 7.8   | 728   | 2      | S43606 |    | R0725. protein (C    |
| 6          | 175   | 4.7   | 595   | 2      | A43534 |    | Lupus autoantigen    |
| 7          | 161.5 | 4.3   | 600   | 2      | S65788 |    | Ku antigen 70K chain |
| 8          | 150.5 | 4.0   | 629   | 2      | S54567 |    | hypothetical prote   |
| 9          | 146.5 | 3.9   | 1055  | 2      | H64577 |    | type I restriction   |
| 10         | 145   | 3.9   | 607   | 2      | T40906 |    | probable ATP-depen   |
| 11         | 143.5 | 3.8   | 1356  | 2      | S32763 |    | kinectin 1 - human   |
| 12         | 142   | 3.8   | 602   | 2      | S54591 |    | DNA-binding factor   |
| 13         | 141   | 3.7   | 1939  | 2      | T18372 |    | repeat organellar    |
| 14         | 138   | 3.7   | 1300  | 2      | I53799 |    | CG1 protein - huma   |
| 15         | 135   | 3.6   | 2094  | 2      | S33124 |    | tpr protein - huma   |
| 16         | 135   | 3.6   | 1496  | 2      | T00499 |    | probable retroelem   |
| 17         | 134   | 3.6   | 1927  | 2      | G64585 |    | cag pathogenicity    |
| 18         | 134   | 3.6   | 2166  | 2      | G70163 |    | hypothetical prote   |
| 19         | 132.5 | 3.5   | 871   | 2      | S97035 |    | DNA polymerase I,    |
| 20         | 132   | 3.5   | 1440  | 2      | T33813 |    | hypothetical prote   |
| 21         | 132   | 3.5   | 1642  | 2      | T08880 |    | NMDA receptor-bind   |
| 22         | 131   | 3.5   | 609   | 2      | A30894 |    | 70K thyroid autoan   |
| 23         | 131   | 3.5   | 950   | 2      | A71655 |    | hypothetical prote   |
| 24         | 129   | 3.4   | 607   | 2      | D86305 |    | hypothetical prote   |
| 25         | 129   | 3.4   | 1087  | 2      | T30320 |    | gelolin-related p    |
| 26         | 129   | 3.4   | 1538  | 2      | T29095 |    | cardiac muscle fac   |
| 27         | 127.5 | 3.4   | 990   | 2      | H88733 |    | protein F32E10.3     |
| 28         | 127   | 3.4   | 904   | 2      | T38806 |    | hypothetical prote   |
| 29         | 127   | 3.4   | 1837  | 2      | T41023 |    | probable nuclear p   |

#### ALIGNMENTS

|   |    |       |     |      |   |                    |
|---|----|-------|-----|------|---|--------------------|
| Copyright (C) 1993 - 2005 Compugen Ltd. | 30 | 127   | 3.4 | 2401 | 2 | T28676             |
|   | 31 | 126.5 | 3.4 | 910  | 2 | S4059              |
|   | 32 | 126.5 | 3.4 | 1295 | 2 | T24587             |
|   | 33 | 126   | 3.4 | 1076 | 2 | C70007             |
|   | 34 | 126   | 3.4 | 2469 | 2 | H36812             |
|   | 35 | 125   | 3.3 | 1222 | 2 | S56030             |
|   | 36 | 125   | 3.3 | 1819 | 2 | A71928             |
|   | 37 | 124.5 | 3.3 | 759  | 2 | topoisomerase IV s |
|   | 38 | 124.5 | 3.3 | 939  | 2 | transport protein  |
|   | 39 | 124.5 | 3.3 | 1790 | 2 | myosin-3 heavy cha |
|   | 40 | 124.5 | 3.3 | 2104 | 2 | P15 protein homol  |
|   | 41 | 124   | 3.3 | 819  | 2 | large segment pro  |
|   | 42 | 124   | 3.3 | 2471 | 2 | probable glucose-6 |
|   | 43 | 123.5 | 3.3 | 550  | 2 | probable membrane  |
|   | 44 | 123.5 | 3.3 | 1178 | 2 | myosin heavy chain |
|   | 45 | 123   | 3.3 | 2139 | 2 |                    |

#### RESULT 1

A32626

Ku antigen 80K chain - human  
 N;Alternate names: CTC 85 protein; DNA-dependent ATPase 83k chain; Ku autoantigen; nucl.

C;Species: Homo sapiens (man)  
 C;Date: 21-May-1990 #sequence revision 21-May-1990 #text change 09-Jul-2004

C;Accession: A35051; A32626; JH0322; A39235; C42397; S54273; A54197  
 R;Mimori, T.; Ohsone, Y.; Hama, N.; Suwa, A.; Akiuti, M.; Honma, M.; Griffith, A.J.; I  
 Proc. Natl. Acad. Sci. U.S.A. 87, 1777-1781, 1990

A;Title: Isolation and characterization of cDNA encoding the 80-kDa subunit protein of

lap syndrome.  
 A;Reference number: A35051; MUID:90175380; PMID:2308937

A;Accession: A35051

A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-732 [MIM: A;Cross-references: UNIPROT:P13010; GB:M30938; NID:9186793; PID:AAA36154.1; PMID:930709.

R;Panayev, M.; Wen, J.; Ayala, A.; Cook, R.  
 J. Biol. Chem. 264, 13407-13411, 1989  
 J. Biol. Chem. 265, 1791-1792, 1990

A;Title: cDNA-derived amino acid sequence of the 86-kDa subunit of the Ku antigen.  
 A;Reference number: A32626; MUID:89340410; PMID:2760028

A;Accession: A32626  
 A;Molecule type: mRNA  
 A;Residues: 1-732 [MIM: A;Cross-references: GB:J04977; NID:9186791; PID:AAA39475.1; PMID:9307093

A;Experimental source: strain NTerA 2D1  
 R;Suives, M.H.; Coenjaerts, F.B.J.; van der Vliet, P.C.  
 J. Exp. Med. 172, 1049-1054, 1990

A;Title: The autoantigen Ku is indistinguishable from NF IV, a protein forming multimer.  
 A;Reference number: JH0322; MUID:9101245; PMID:212941  
 A;Accession: JH0322

A;Molecule type: mRNA  
 A;Residues: 105-732 <STP>  
 A;Accession: A39235

A;Molecule type: protein  
 A;Residues: 2-12, X', 14-22 <RNU>  
 R;Wojciechowski, A.; Henzel, W.; Huston, L.; Paslidis, N.; Ellerson, D.; McRae, M.; Seon

J. Biol. Chem. 267, 4533-4540, 1992  
 A;Title: Identification of proteins binding to interferon-inducible transcriptional enh.

A;Reference number: A42397; MUID:92165807; PMID:1537839  
 A;Accession: C42397

A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 526-565 <WBD>  
 A;Experimental source: K562 cells

A;Title: Sequence extracted from NCBI backbone (NCBIP:85281)  
 R;Generich, B.; Bckerskorn, C.; Lottspeich, F.; Herzog, C.; Kuehn, K.; Poeschl, E.

GenCore version 5.1.6  
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 17, 2005, 20:15:42 ; Search time 166 Seconds

1 MVRSGRNKAAVVLCLMVGPTM.....GDTAAVFERGGDVDDLLDM1 732  
 (without alignments)  
 1726.753 Million cell updates/sec

Title: US-10-768-030-1  
 Perfect score: 3761  
 Sequence: 1 MVRSGRNKAAVVLCLMVGPTM.....GDTAAVFERGGDVDDLLDM1 732

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications AA.\*  
 1: /cgn2\_6\_ptodata/2/pubpaa/US07\_PUBCOMB.pep: \*  
 2: /cgn2\_6\_ptodata/2/pubpaa/US07\_PUBCOMB.pep: \*  
 3: /cgn2\_6\_ptodata/2/pubpaa/US06\_NEW\_PUB.pep: \*  
 4: /cgn2\_6\_ptodata/2/pubpaa/US06\_PUBCOMB.pep: \*  
 5: /cgn2\_6\_ptodata/2/pubpaa/US07\_NEW\_PUB.pep: \*  
 6: /cgn2\_6\_ptodata/2/pubpaa/PCRTS\_PUBCOMB.pep: \*  
 7: /cgn2\_6\_ptodata/2/pubpaa/PCRTS\_PUBCOMB.pep: \*  
 8: /cgn2\_6\_ptodata/2/pubpaa/US08\_NEW\_PUB.pep: \*  
 9: /cgn2\_6\_ptodata/2/pubpaa/US09\_PUBCOMB.pep: \*  
 10: /cgn2\_6\_ptodata/2/pubpaa/US09\_PUBCOMB.pep: \*  
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 13: /cgn2\_6\_ptodata/2/pubpaa/US10A\_PUBCOMB.pep: \*  
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 20: /cgn2\_6\_ptodata/2/pubpaa/US11\_NEW\_PUB.pep: \*  
 21: /cgn2\_6\_ptodata/2/pubpaa/US60\_NEW\_PUB.pep: \*  
 22: /cgn2\_6\_ptodata/2/pubpaa/US60\_PUBCOMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match Length | DB ID  | Description                            |
|------------|--------|--------------------|--------|--|
| 1          | 3761   | 100.0              | 732 14 | US-10-097-340-363 Sequence 363, APP    |
| 2          | 3761   | 100.0              | 732 15 | US-10-116-275-169 Sequence 169, APP    |
| 3          | 3761   | 100.0              | 732 16 | US-10-408-768A-1124 Sequence 1124, APP |
| 4          | 3761   | 100.0              | 732 17 | US-10-768-030-1 Sequence 1, APP        |
| 5          | 3761   | 100.0              | 741 9  | US-09-833-790-432 Sequence 432, APP    |
| 6          | 3756   | 99.9               | 731 14 | US-10-160-748-7 Sequence 7, APP        |
| 7          | 2971   | 79.0               | 732 14 | US-10-160-748-4 Sequence 4, APP        |
| 8          | 2891   | 79.0               | 732 14 | US-10-160-748-5 Sequence 5, APP        |
| 9          | 2893   | 76.9               | 732 14 | US-10-160-748-6 Sequence 6, APP        |
| 10         | 2545.5 | 67.7               | 521 9  | US-09-805-020-38 Sequence 38, APP      |
| 11         | 2530   | 67.3               | 497 9  | US-09-805-020-37 Sequence 37, APP      |

Sequence 62759, A  
 Sequence 2, APP11  
 Sequence 357314, APP  
 Sequence 113099, APP  
 Sequence 35456, APP  
 Sequence 5634, APP  
 Sequence 37636, APP  
 Sequence 34694, APP  
 Sequence 34542, APP  
 Sequence 548, APP  
 Sequence 13409, APP  
 Sequence 42907, APP  
 Sequence 357315, APP  
 Sequence 18014, APP  
 Sequence 167597, APP  
 Sequence 596, APP  
 Sequence 1922, APP  
 Sequence 3523, APP  
 Sequence 52621, APP  
 Sequence 54545, APP  
 Sequence 278336, APP  
 Sequence 167597, APP  
 Sequence 54564, APP  
 Sequence 1922, APP  
 Sequence 3340, APP  
 Sequence 59, APP1  
 Sequence 766, APP  
 Sequence 257, APP  
 Sequence 2, APP11  
 Sequence 17999, APP  
 Sequence 20654, APP  
 Sequence 357245, APP  
 Sequence 231005, APP  
 Sequence 2096, APP

#### ALIGNMENTS

#### RESULT 1

US-10-097-340-363

; Sequence 363, Application US/10097340  
 ; Publication No. US20030087250A1  
 ; GENERAL INFORMATION:

; APPLICANT: John MONAHAN

; APPLICANT: Manjula GANNAVARAMU

; APPLICANT: Sebastian HOERSCH

; APPLICANT: Shubhangi KAMATKAR

; APPLICANT: Steve G. KOVATS

; APPLICANT: Rachel B. MEYERS

; APPLICANT: Michael MORRISSEY

; APPLICANT: Peter OLANDT

; APPLICANT: Ami SEN

; APPLICANT: Peter VEIBY

; APPLICANT: Gordon B. MILLS

; APPLICANT: Robert C. EAST, JR.

; APPLICANT: Karen LIU

; APPLICANT: Rosemarie SCHMIDT

; APPLICANT: Xumei ZHAO

; APPLICANT: Karen GLATT

; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,

; FILE REFERENCE: MRI-030

; CURRENT FILING DATE: 2002-03-14

; PRIORITY APPLICATION NUMBER: 60/276,025

; PRIORITY FILING DATE: 2001-03-14

; PRIORITY APPLICATION NUMBER: 60/325,149

; PRIORITY FILING DATE: 2001-09-26

; PRIORITY APPLICATION NUMBER: 60/276,026

; PRIORITY FILING DATE: 2001-03-14

; PRIORITY APPLICATION NUMBER: 60/324,967

; PRIORITY FILING DATE: 2001/09/26

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GenCore version 5.1.6

OM protein - protein search, using SW model

Run on: August 17, 2005, 20:11:01 ; Search time 24 Seconds

(without alignments)

2276.796 Million cell updates/sec

Title: US-10-768-030-1

Perfect score: 3761

Sequence: 1 MVRSGENKAAVYLCKMVGFTM. .... GDTAAVFEEGGDVDDLLDMI 732

Scoring table: BLOSUM62

Gapext 0.5

Scanned: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Maximum Match 0\*

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cggn2\_6/ptodata/1/1aa/5A-COMB.pep:\*

2: /cmn2\_6/ptodata/1/1aa/5B-COMB.pep:\*

3: /cggn2\_6/ptodata/1/1aa/6A-COMB.pep:\*

4: /cggn2\_6/ptodata/1/1aa/6B-COMB.pep:\*

5: /cmn2\_6/ptodata/1/1aa/PCFTUS-COMB.pep:\*

6: /cggn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID                 | Description           |
|------------|-------|-------------|--------|-----------------------|-----------------------|
| 1          | 3761  | 100.0       | 732    | 4 US-09-569-037-7     | Sequence 7, Appli     |
| 2          | 3761  | 100.0       | 732    | 4 US-09-569-037-7     | Sequence 7000, Appli  |
| 3          | 3761  | 100.0       | 743    | 4 US-09-569-037-7     | Sequence 1112, Appli  |
| 4          | 3756  | 99.9        | 731    | 4 US-10-160-748-7     | Sequence 2, Appli     |
| 5          | 3730  | 99.2        | 820    | 3 US-09-173-914-2     | Sequence 4, Appli     |
| 6          | 2971  | 79.0        | 732    | 4 US-10-160-748-4     | Sequence 5, Appli     |
| 7          | 2971  | 79.0        | 732    | 4 US-10-160-748-5     | Sequence 6, Appli     |
| 8          | 2893  | 76.9        | 732    | 4 US-10-160-748-6     | Sequence 5706, Appli  |
| 9          | 700   | 18.6        | 137    | 4 US-09-513-939-5     | Sequence 2, Appli     |
| 10         | 543   | 14.4        | 681    | 4 US-10-160-748-2     | Sequence 16, Appli    |
| 11         | 394   | 10.5        | 78     | 4 US-09-569-037-16    | Sequence 17, Appli    |
| 12         | 314.5 | 8.4         | 77     | 4 US-09-569-037-17    | Sequence 18, Appli    |
| 13         | 314.5 | 8.4         | 77     | 4 US-09-569-037-18    | Sequence 9, Appli     |
| 14         | 294.5 | 7.8         | 728    | 4 US-09-569-037-11    | Sequence 11, Appli    |
| 15         | 174   | 4.6         | 34     | 4 US-09-569-037-4     | Sequence 4, Appli     |
| 16         | 161.5 | 4.3         | 600    | 4 US-09-569-037-4     | Sequence 9, Appli     |
| 17         | 150.5 | 4.0         | 629    | 4 US-09-569-037-9     | Sequence 6, Appli     |
| 18         | 141   | 3.7         | 602    | 4 US-09-569-037-6     | Sequence 19139, Appli |
| 19         | 139.5 | 3.7         | 531    | 4 US-09-569-037-18    | Sequence 7561, Appli  |
| 20         | 138   | 3.7         | 1307   | 4 US-09-569-037-8     | Sequence 2, Appli     |
| 21         | 137.5 | 3.7         | 650    | 3 US-09-569-037-11    | Sequence 10828, Appli |
| 22         | 135.5 | 3.6         | 2186   | 4 US-09-569-037-4     | Sequence 914, Appli   |
| 23         | 135.5 | 3.6         | 2349   | 4 US-09-538-092-914   | Sequence 126, Appli   |
| 24         | 131   | 3.5         | 608    | 3 US-08-160-107A-126  | Sequence 2, Appli     |
| 25         | 131   | 3.5         | 609    | 4 US-09-569-037-2     | Sequence 5178, Appli  |
| 26         | 130   | 3.5         | 1010   | 3 US-09-134-001C-5178 | Sequence 116, Appli   |
| 27         | 129.5 | 3.4         | 2871   | 4 US-09-538-092-916   | Sequence 14866, Appli |

## ALIGNMENTS

RESULT 1

US-09-569-037-7

; Sequence 7, Application US/09569037

; Patent No. 6753151

; GENERAL INFORMATION:

; APPLICANT: Jackson, Stephen P

; TITLE OF INVENTION: Interactions of Ku polypeptides and applications

; FILE REFERENCE: 620-100

; CURRENT APPLICATION NUMBER: US/09/569,037

; PRIOR APPLICATION NUMBER: PCT/GB00/01245

; PRIOR FILING DATE: 2000-05-11

; PRIOR APPLICATION NUMBER: GB 9907667.9

; PRIOR FILING DATE: 1999-04-01

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 732

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-569-037-7

Query Match 100.0%; Score 3761; DB 4; Length 732;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVRSGENKAAVYLCKMVGFTMMSNSIIGIESSPREQAKVITMIVQRQYFAENKDEILAVLFG 60

Db 1 MVRSGENKAAVYLCKMVGFTMMSNSIIGIESSPREQAKVITMIVQRQYFAENKDEILAVLFG 60

Qy 61 TDGTINPLSLGGDQDQITVHRLMPDFDILEDISKIQPGSQODDFLDALIVSDVHQH 120

Db 61 TDGTINPLSLGGDQDQITVHRLMPDFDILEDISKIQPGSQODDFLDALIVSDVHQH 120

Qy 121 ETIGKFKERKHTETTDLSRFSKQOLDIITHSLRKCDISLQOFFLPPSLGGDQEDGSGDGRQD 180

Db 121 ETIGKFKERKHTETTDLSRFSKQOLDIITHSLRKCDISLQOFFLPPSLGGDQEDGSGDGRQD 180

Qy 241 ERHSIHWPCLTIGNSLIRIATKTSILQERVKRTTWDKTLKEDIQETVYCLND 300

Db 241 ERHSIHWPCLTIGNSLIRIATKTSILQERVKRTTWDKTLKEDIQETVYCLND 300

Qy 301 DETEVTKEDIQGFGYGSIDIVPSKVDDEQMKYKSEGKCFSVLGFCKSSQYQRFPMGNQ 360

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: August 17, 2005, 20:08:01 ; Search time 165 Seconds  
(without alignments)

Perfect score: 3761 ; Total score: 1715.810 Million cell updates/sec

Title: US-10-768-030-1

Scoring table: BLOSUM62

Gapop: 10.0 , Gapext: 0.5

Sequence: MVRSGNKAAVVLCMDVGPTM.....GDTAAVFFEGGDVDDILDMDI 732

Post-processing: Minimum Match 100% ; Maximum Match 100% ; Listing First 45 Summaries

Database : A\_Geneseq\_16Dec04:\*

1: GeneseqP1980:\*

2: GeneseqP1990:\*

3: GeneseqP2000:\*

4: GeneseqP2001:\*

5: GeneseqP2002:\*

6: GeneseqP2003as:\*

7: GeneseqP2003bs:\*

8: GeneseqP2004as:\*

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100% ; Maximum Match 100% ; Listing First 45 Summaries

Score: 2105692

Total number of hits satisfying chosen parameters: 2105692

Score: 2105692  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 100% ; Maximum Match 100% ; Listing First 45 Summaries

Result No. Score Query Match Length DB ID

1 3761 100.0 732 5 ABGG9652 Human ova  
2 3761 100.0 732 7 ADJ69318 Human ha  
3 3761 100.0 732 8 ADP43915 Human DNA  
4 3761 100.0 732 8 ADQ14382 Human lup  
5 3761 100.0 732 8 ABm80379 Tumour-as  
6 3761 100.0 732 8 ADR97394 Human XRC  
7 3761 100.0 732 8 ADS14356 Human lup  
8 3761 100.0 741 5 AAu69427 Lung small  
9 3756 99.9 731 8 ADJ66474 ATP-Depen  
10 3754 99.8 732 8 ADR41763 Protein d  
11 3688 98.2 732 4 AAB66590 Human Ku8  
12 3688 98.1 732 4 AAB29307 Human Ku8  
13 3354 89.2 757 4 ABG08315 Novel hum  
14 3221 85.6 628 6 ABU07475 Protein d  
15 2893 76.9 732 6 AAW40496  
16 2545.5 67.7 521 5 ABG79671 Tumour in  
17 2530 67.3 497 5 ABG79670 Tumour in  
18 2454 65.2 644 2 AAW40497  
19 1784 47.4 384 4 ABG08312 Novel hum  
20 1034.5 27.5 710 4 ABG08311 Novel hum  
21 926.5 24.6 210 6 ABG9983 Human nov  
22 700 18.6 137 3 AAG01625 Human sec  
23 658 17.5 138 4 ABG08310 Novel hum  
24 543 14.4 681 3 AAB19283 Amino aci  
25 489 13.0 132 3 ARB44085 Human can

## ALIGNMENTS

RESULT 1  
ID ABG36452 standard; protein; 732 AA.

AC ABG36452;

XX 11-DEC-2002 (first entry)

XX Human ovarian cancer marker M480.

XX DE Human ovarian cancer marker M480.

XX KW Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; non-tuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker.

XX KW Homo sapiens.

XX WO200271928-A2.

OS PN

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Match Length DB ID Description

1 3761 100.0 732 5 ABGG9652 Human ova  
2 3761 100.0 732 7 ADJ69318 Human ha  
3 3761 100.0 732 8 ADP43915 Human DNA  
4 3761 100.0 732 8 ADQ14382 Human lup  
5 3761 100.0 732 8 ABm80379 Tumour-as  
6 3761 100.0 732 8 ADR97394 Human XRC  
7 3761 100.0 732 8 ADS14356 Human lup  
8 3761 100.0 741 5 AAu69427 Lung small  
9 3756 99.9 731 8 ADJ66474 ATP-Depen  
10 3754 99.8 732 8 ADR41763 Protein d  
11 3688 98.2 732 4 AAB66590 Human Ku8  
12 3688 98.1 732 4 AAB29307 Human Ku8  
13 3354 89.2 757 4 ABG08315 Novel hum  
14 3221 85.6 628 6 ABU07475 Protein d  
15 2893 76.9 732 6 AAW40496  
16 2545.5 67.7 521 5 ABG79671 Tumour in  
17 2530 67.3 497 5 ABG79670 Tumour in  
18 2454 65.2 644 2 AAW40497  
19 1784 47.4 384 4 ABG08312 Novel hum  
20 1034.5 27.5 710 4 ABG08311 Novel hum  
21 926.5 24.6 210 6 ABG9983 Human nov  
22 700 18.6 137 3 AAG01625 Human sec  
23 658 17.5 138 4 ABG08310 Novel hum  
24 543 14.4 681 3 AAB19283 Amino aci  
25 489 13.0 132 3 ARB44085 Human can

(MILL-) MILLENNIUM PHARM INC. PI Monahan JB, Gannavarapu M, Hoerich S, Kamatkar S, Kovatis SG; PI Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vieby PO, Mills GB; PI Basic RC, Lu K, Schmandt RE, Zhao X, Glatt K; DR WPI: 2002-723277/78. DR N-PSDB; ABS76552.

Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient.